

Saidha

#5

1653

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/628,693

DATE: 08/28/2001

TIME: 08:20:34

Input Set : A:\34950193.app

Output Set: N:\CRF3\00202001\I628693.raw

ENTERED

3 <110> APPLICANT: Haroche, Julien
4 Allignet, Jeanine
5 El Solh, Nevine
7 <120> TITLE OF INVENTION: DETECTION OF A GENE, vatD, ENCODING AN ACETYLTRANSFERASE
8 INACTIVATING STREPTOGRAMIN
10 <130> FILE REFERENCE: 03495.0193
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/628,693
C--> 13 <141> CURRENT FILING DATE: 2000-07-28
15 <160> NUMBER OF SEQ ID NOS: 22
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 213
21 <212> TYPE: PRT
22 <213> ORGANISM: Enterococcus faecium
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26 1 5 10 15
28 Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile
29 20 25 30
31 Gly Asp Tyr Thr Tyr Tyr Asp Asp Pro Val Asn Pro Thr Asp Phe Glu
32 35 40 45
34 Lys His Val Thr His His Tyr Glu Phe Leu Gly Asp Lys Leu Ile Ile
35 50 55 60
37 Gly Lys Phe Cys Ser Leu Ala Ser Gly Ile Glu Phe Ile Met Asn Gly
38 65 70 75 80
40 Ala Asn His Val Met Lys Gly Ile Ser Thr Tyr Pro Phe Asn Ile Leu
41 85 90 95
43 Gly Gly Asp Trp Gln Gln Tyr Thr Pro Glu Leu Thr Asp Leu Pro Leu
44 100 105 110
46 Lys Gly Asp Thr Val Val Gly Asn Asp Val Trp Phe Gly Gln Asn Val
47 115 120 125
49 Thr Val Leu Pro Gly Val Lys Ile Gly Asp Gly Ala Ile Ile Gly Ala
50 130 135 140
52 Asn Ser Val Val Thr Lys Asp Val Ala Pro Tyr Thr Ile Val Gly Gly
53 145 150 155 160
55 Asn Pro Ile Gln Leu Ile Gly Pro Arg Phe Glu Pro Glu Val Ile Gln
56 165 170 175
58 Ala Leu Glu Asn Leu Ala Trp Trp Asn Lys Asp Ile Glu Trp Ile Thr
59 180 185 190
61 Ala Asn Val Pro Lys Leu Met Gln Thr Thr Pro Thr Leu Glu Leu Ile
62 195 200 205
64 Asn Ser Leu Met Glu
65 210
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 642
70 <212> TYPE: DNA
71 <213> ORGANISM: Enterococcus faecium

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73 <400> SEQUENCE: 2

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74 atgactatac ctgacgcaaa tgcaatctat cataactcag ccatacaaaga gggtgtcttt 60
75 atcaagaacg tgatcaaaaag tccaatatt gaaattgggg actacaccta ttatgatgac 120
76 ccagtaaatc ccaccgattt iyagaaacac gttaccatc actatgaatt tctaggcgac 180
77 aaattaatca toggtaaatt ttgttctctc gccagtggca ttgaatttat catgaacggt 240
78 gccaacacag taatgaaagg tatttcgact tatccattta atatattagg tggcgattgg 300
79 caacaatata ctctgaact gactgatttg ccgttgaaag gtgatactgt agtcggaaat 360
80 gacgtgtggt ttgggcaaaa tgtgaccgtc ctaccaggcg taaaaatagg tgacggtgcc 420
81 attatcggag caaatagtgt tgtaacaaaa gacgtcgctc catatacaat tgtcggtggc 480
82 aatccaattc aactcatcgg accaagattt gaaccggaag ttattcaagc attagaaaaat 540
83 ctggcatggt ggaataaaga tattgaatgg ataactgcta atgttcctaa actaatgcaa 600
84 acaacaccca cacttgaatt gataaacagt ttaatggaaa aa 642

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87 <210> SEQ ID NO: 3

88 <211> LENGTH: 25

89 <212> TYPE: DNA

90 <213> ORGANISM: Artificial Sequence

92 <220> FEATURE:

93 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

95 <400> SEQUENCE: 3

96 caatattgga attcgggact acacc 25

99 <210> SEQ ID NO: 4

100 <211> LENGTH: 22

101 <212> TYPE: DNA

102 <213> ORGANISM: Artificial Sequence

104 <220> FEATURE:

105 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

107 <400> SEQUENCE: 4

108 ctgtttatga attcaagtgt gg 22

111 <210> SEQ ID NO: 5

112 <211> LENGTH: 7

113 <212> TYPE: PRT

114 <213> ORGANISM: Enterococcus faecium

116 <400> SEQUENCE: 5

117 Ile Met Asn Gly Ala Asn His

118 1 5

121 <210> SEQ ID NO: 6

122 <211> LENGTH: 18

123 <212> TYPE: DNA

124 <213> ORGANISM: Artificial Sequence

126 <220> FEATURE:

127 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

129 <220> FEATURE:

130 <223> OTHER INFORMATION: "n" bases may be a, t, c or g

132 <400> SEQUENCE: 6

133 athatgaayg cnaaycay 18

136 <210> SEQ ID NO: 7

137 <211> LENGTH: 5

138 <212> TYPE: PRT

139 <213> ORGANISM: Enterococcus faecium

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Input Set : A:\34950193.app

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141 <400> SEQUENCE: 7
 142 Gly Asn Asp Val Trp
 143 1 5
 146 <210> SEQ ID NO: 8
 147 <211> LENGTH: 15
 148 <212> TYPE: DNA
 149 <213> ORGANISM: Artificial Sequence
 151 <220> FEATURE:
 152 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 154 <220> FEATURE:
 155 <223> OTHER INFORMATION: "n" bases may be a, t, c or g
 157 <400> SEQUENCE: 8
 158 ccacacrtcr ttnc 15
 161 <210> SEQ ID NO: 9
 162 <211> LENGTH: 8
 163 <212> TYPE: PRT
 164 <213> ORGANISM: Enterococcus faecium
 166 <400> SEQUENCE: 9
 167 Ala Asn Ala Ile Tyr His Asn Ser
 168 1 5
 171 <210> SEQ ID NO: 10
 172 <211> LENGTH: 24
 173 <212> TYPE: DNA
 174 <213> ORGANISM: Enterococcus faecium
 176 <400> SEQUENCE: 10
 177 gcaaagtcaa tctatcataa ctca 24
 180 <210> SEQ ID NO: 11
 181 <211> LENGTH: 9
 182 <212> TYPE: PRT
 183 <213> ORGANISM: Enterococcus faecium
 185 <400> SEQUENCE: 11
 186 Met Gln Thr Thr Pro Thr Leu Glu Leu
 187 1 5
 190 <210> SEQ ID NO: 12
 191 <211> LENGTH: 27
 192 <212> TYPE: DNA
 193 <213> ORGANISM: Enterococcus faecium
 195 <400> SEQUENCE: 12
 196 atgcaaacaa caccacact tgaattg 27
 199 <210> SEQ ID NO: 13
 200 <211> LENGTH: 23
 201 <212> TYPE: DNA
 202 <213> ORGANISM: Artificial Sequence
 204 <220> FEATURE:
 205 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 207 <400> SEQUENCE: 13
 208 tagaaagaat tcagtgattg tgg 23
 211 <210> SEQ ID NO: 14
 212 <211> LENGTH: 26

RAW SEQUENCE LISTING

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213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
219 <400> SEQUENCE: 14
220 ggattcacta aatagtaaag gccgtg 26
223 <210> SEQ ID NO: 15
224 <211> LENGTH: 840
225 <212> TYPE: DNA
226 <213> ORGANISM: Enterococcus faecium
228 <400> SEQUENCE: 15
229 aaatttaggc gcacaaaaag aaagagtgtg acaaaacatg gttatgctac atgtttaagg 60
230 taaaaatagt tatgtcacia ctacttattt ttttacccaa tcttctagac tataattaaa 120
231 attaaataac tcaattcggg ggtactaacc tgactatacc tgacgcaa at gcaatctatc 180
232 ataactcagc catcaaagag gttgacttta tcaagaacgt gatcaaaagt cccaatattg 240
233 aaattgggga ctacacctat tatgatgacc cagtaa atcc caccgatttt gagaaacacg 300
234 ttacccatca ctatgaattt ctaggcgaca aattaatcat cggtaa attt tgttctctcg 360
235 ccagtggcat tgaattttatc atgaacgggtg ccaaccacgt aatgaa aggt atttcgactt 420
236 atccatttaa tatattaggt ggcgattggc aacaatacac tcctgaactg actgatttgc 480
237 cgttgaaaag tgatactgta gtcggaaatg acgtgtggtt tgggcaaa at gtgaccgtcc 540
238 taccaggcgt aaaaataggt gacggtgcc a ttatcggagc aaatagtgtt gtaacaaa ag 600
239 acgtcgctcc atatacaatt gtcggtggca atccaattca actcatcgga ccaagatttg 660
240 aaccggaagt tattcaagca ttagaaaatc tggcatgggt gaataa agat attgaatgga 720
241 taactgctaa tgttcctaaa ctaatgcaa caacacccac acttgaattg ataaacagtt 780
242 taatggaaaa ataaaaacaa aaaagccgtg caagcaatcc aaaaatgatt gtttacacgg 840
245 <210> SEQ ID NO: 16
246 <211> LENGTH: 44
247 <212> TYPE: DNA
248 <213> ORGANISM: Enterococcus faecium
250 <400> SEQUENCE: 16
251 tgtcacaact acttattttt ttacccaatc ttctagacta taat 44
254 <210> SEQ ID NO: 17
255 <211> LENGTH: 1080
256 <212> TYPE: DNA
257 <213> ORGANISM: Enterococcus faecium
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (271)..(912)
263 <400> SEQUENCE: 17
264 ccctttaaag agggctttta tatattaatc acaaatcact tatcacia at cacaagtgat 60
266 ttgtgattgt tgatgataaa ataagaataa gaagaaatag aaagaagtga gtgattgtgg 120
268 gaaatttagg cgcacaaaaa gaaagagtgt gacaaaacat ggttatgcta catgtttaag 180
270 gtaaaaatag ttatgtcaca actacttatt tttttacca atcttctaga ctataattaa 240
272 aattaaataa ctcaattcgg aggtactaac atg act ata cct gac gca aat gca 294
273 Met Thr Ile Pro Asp Ala Asn Ala
274 1 5
276 atc tat cat aac tca gcc atc aaa gag gtt gtc ttt atc aag aac gtg 342
277 Ile Tyr His Asn Ser Ala Ile Lys Glu Val Val Phe Ile Lys Asn Val
278 10 15 20

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280 atc aaa agt ccc aat att gaa att ggg gac tac acc tat tat gat gac 390
281 Ile Lys Ser Pro Asn Ile Glu Ile Gly Asp Tyr Thr Tyr Tyr Asp Asp
282 25 30 35 40
284 cca gta aat ccc acc gat ttt gag aaa cac gtt acc cat cac tat gaa 438
285 Pro Val Asn Pro Thr Asp Phe Glu Lys His Val Thr His His Tyr Glu
286 45 50 55
288 ttt cta ggc gac aaa tta atc atc ggt aaa ttt tgt tct ctc gcc agt 486
289 Phe Leu Gly Asp Lys Leu Ile Ile Gly Lys Phe Cys Ser Leu Ala Ser
290 60 65 70
292 ggc att gaa ttt atc atg aac ggt gcc aac cac gta atg aaa ggt att 534
293 Gly Ile Glu Phe Ile Met Asn Gly Ala Asn His Val Met Lys Gly Ile
294 75 80 85
296 tcg act tat cca ttt aat ata tta ggt ggc gat tgg caa caa tac act 582
297 Ser Thr Tyr Pro Phe Asn Ile Leu Gly Gly Asp Trp Gln Gln Tyr Thr
298 90 95 100
300 cct gaa ctg act gat ttg ccg ttg aaa ggt gat act gta gtc gga aat 630
301 Pro Glu Leu Thr Asp Leu Pro Leu Lys Gly Asp Thr Val Val Gly Asn
302 105 110 115 120
304 gac gtg tgg ttt ggg caa aat gtg acc gtc cta cca ggc gta aaa ata 678
305 Asp Val Trp Phe Gly Gln Asn Val Thr Val Leu Pro Gly Val Lys Ile
306 125 130 135
308 ggt gac ggt gcc att atc gga gca aat agt gtt gta aca aaa gac gtc 726
309 Gly Asp Gly Ala Ile Ile Gly Ala Asn Ser Val Val Thr Lys Asp Val
310 140 145 150
312 gct cca tat aca att gtc ggt ggc aat cca att caa ctc atc gga cca 774
313 Ala Pro Tyr Thr Ile Val Gly Gly Asn Pro Ile Gln Leu Ile Gly Pro
314 155 160 165
316 aga ttt gaa ccg gaa gtt att caa gca tta gaa aat ctg gca tgg tgg 822
317 Arg Phe Glu Pro Glu Val Ile Gln Ala Leu Glu Asn Leu Ala Trp Trp
318 170 175 180
320 aat aaa gat att gaa tgg ata act gct aat gtt cct aaa cta atg caa 870
321 Asn Lys Asp Ile Glu Trp Ile Thr Ala Asn Val Pro Lys Leu Met Gln
322 185 190 195 200
324 aca aca ccc aca ctt gaa ttg ata aac agt tta atg gaa aaa 912
325 Thr Thr Pro Thr Leu Glu Leu Ile Asn Ser Leu Met Glu Lys
326 205 210
328 taaaaacaaa aaagccgtgc aagcaatcca aaaatgattg tttacacggc ctttactatt 972
330 tagtgaatcc aattttattaa taatagatat gatataccag taaaaaatac actagccacc 1032
332 tctggcggta ctctactcgt atattttatt tacgaccttc tgatgata 1080
335 <210> SEQ ID NO: 18
336 <211> LENGTH: 214
337 <212> TYPE: PRT
338 <213> ORGANISM: Enterococcus faecium
340 <400> SEQUENCE: 18
341 Met Thr Ile Pro Asp Ala Asn Ala Ile Tyr His Asn Ser Ala Ile Lys
342 1 5 10 15
344 Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile
345 20 25 30
347 Gly Asp Tyr Thr Tyr Tyr Asp Asp Pro Val Asn Pro Thr Asp Phe Glu

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VERIFICATION SUMMARY

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Input Set : A:\34950193.app

Output Set: N:\CRF3\08282001\I628693.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:133 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:133 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:158 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:158 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8